Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (Original) A method for displaying genotype information associated with probe array experiments, comprising the acts of:

receiving one or more sets of emission intensity data, wherein each set of emission intensity data includes a plurality of emission intensity values each associated with a probe disposed upon a probe array;

generating a plurality of genotype calls, wherein each of the genotype calls is based, at least in part, upon one or more of the emission intensity values;

assembling the plurality of genotype calls into one or more genotype data sets; and

displaying each of the one or more genotype data sets in one or more panes of a graphical user interface.

2. (Original) The method of claim 1, wherein:

each of the plurality of emission intensity values corresponds to detected emissions from a scanned probe array.

3. (Original) The method of claim 1, wherein:

the probe includes a genotyping probe. ·

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4. (Original) The method of claim 3, wherein:

the genotyping probe includes a sequencing probe.

5. (Original) The method of claim 3, wherein:

the genotyping probe includes a SNP probe.

6. (Original) The method of claim 1, wherein:

the genotype call is an A, G, C, T, or (n) call.

7. (Original) The method of claim 1, wherein:

the genotype call includes a SNP call.

8. (Original) The method of claim 1, wherein:

the one or more panes includes a tabular format

9. (Original) The method of claim 1, wherein:

the one or more panes includes a graphical format.

10. (Original) The method of claim 8, wherein:

the graphical format includes a representation of relative SNP call quality.

11. (Original) The method of claim 8, wherein:

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the graphical format includes the plurality of genotype calls associated with a

representation of a sequence.

12. (Original) The method of claim 8, wherein:

the graphical format includes a representation of probe intensity.

13. (Original) The method of claim 1, further comprising the acts of:

retrieving annotation information in response to a user selection of one or more of

the displayed genotype calls; and

displaying the annotation information in one or more panes of the graphical user

interface.

14. (Original) A system for displaying genotype information associated with probe

array experiments, comprising:

a sequence data manager constructed and arranged to receive one or more sets of

emission intensity data, wherein each set of emission intensity data includes a plurality of

emission intensity values each associated with a probe disposed upon a probe array;

a genotype call generator constructed and arranged to generate a plurality of

genotype calls, wherein each of the genotype calls is based, at least in part, upon one or

more of the emission intensity values;

a data assembler constructed and arranged to assemble the plurality of genotype

calls into one or more genotype data sets; and

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an output manager constructed and arranged to display each of the one or more

genotype data sets in one or more panes of a graphical user interface.

15.   (Original) The system of claim 14, wherein:

each of the plurality of emission intensity values corresponds to detected

emissions from a scanned probe array.

16.   (Original) The system of claim 14, wherein:

the probe includes a genotyping probe.

17.   (Original) The system of claim 16, wherein:

the genotyping probe includes a sequencing probe.

18.   (Original) The system of claim 16, wherein:

the genotyping probe includes a SNP probe.

19.   (Original) The system of claim 14, wherein:

the genotype call is an A, G, C, T, or (n) call.

20.   (Original) The system of claim 14, wherein:

the genotype call includes a SNP call.

21.   (Original) The system of claim 14, wherein:

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the one or more panes includes a tabular format

22. (Original) The system of claim 14, wherein:

the one or more panes includes a graphical format.

23. (Original) The system of claim 22, wherein:

the graphical format includes a representation of relative SNP call quality.

24. (Original) The system of claim 22, wherein:

the graphical format includes the plurality of genotype calls associated with a

representation of a sequence.

25. (Original) The system of claim 22, wherein:

the graphical format includes a representation of probe intensity.

26. (Original) The system of claim 14, wherein:

the output manager is further constructed and arranged to retrieve annotation

information in response to a user selection of one or more of the displayed genotype calls,

and display the annotation information in one or more panes of the graphical user

interface.

27. (Original) A computer system for displaying genotype information associated

with probe array experiments, comprising:

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a user computer having system memory with executable code stored thereon,

wherein the executable code is constructed and arranged to perform the acts of;

receiving one or more sets of emission intensity data, wherein each set of

emission intensity data includes a plurality of emission intensity values each associated

with a probe disposed upon a probe array;

generating a plurality of genotype calls, wherein each of the genotype calls

is based, at least in part, upon one or more of the emission intensity values;

assembling the plurality of genotype calls into one or more genotype data

sets; and

displaying each of the one or more genotype data sets in one or more

panes of a graphical user interface.

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